

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-11 (canceled):

Claim 12 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is a gene product whose activity or amount is reduced by an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463, provided that cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claims 13-30 (canceled):

Claim 31 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463 a gene product having at least 25% amino acid

identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected of SEQ ID NO: 1463 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid of SEQ ID NO: 1463; provided that said cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a nonsensitized cell.

Claims 32-44 (canceled):

Claim 45 (previously presented): The method of Claim 31, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 46 (previously presented): The method of Claim 31, wherein said gene product is from an organism other than *E. coli*.

Claim 47 (previously presented): The method of Claim 31, wherein said cell is an organism other than *E. coli*.

Claim 48 (previously presented): The method of Claim 31, wherein said sensitized cell is a pathogenic microorganism.

Claim 49 (previously presented): The method of Claim 31, wherein said sensitized cell is a Gram positive bacterium.

Claim 50 (previously presented): The method of Claim 49, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 51 (previously presented): The method of Claim 50, wherein said bacterium is *Staphylococcus aureus*.

Claim 52 (previously presented): The method of Claim 50, wherein said *Staphylococcus* species is coagulase negative.

Claim 53 (previously presented): The method of Claim 51, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 54 (previously presented): The method of Claim 31, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 55 (previously presented): The method of Claim 31, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 56 (previously presented): The method of Claim 31, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 57 (previously presented): The method of Claim 31, wherein said gene product is a polypeptide.

Claim 58 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 99% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 59 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 95% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 60 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 90% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 61 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 85% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 62 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 80% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 63 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 70% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 64 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 60% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 65 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 50% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 66 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 40% amino acid identity as determined using FASTA version 3.0t78 SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 67 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 68 (previously presented): The method of Claim 57, wherein said polypeptide is 12600.

Claim 69 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 34% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 39% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 42% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600 and a polypeptide having at least 43% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600.

Claims 70-76 (canceled):

Claim 77 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product is selected from the group consisting of SEQ ID NOs: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605.

Claim 78 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 97% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 79 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 95% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 80 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 90% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 81 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 85% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 82 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 80% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 83 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 84 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence comprising at least 100 consecutive nucleotides of SEQ ID NO: 1463.

Claim 85 (previously presented): The method of Claim 12, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 86 (previously presented): The method of Claim 12, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enterococcus faecalis*.

Claim 87 (previously presented): The method of Claim 86, wherein said prokaryotic organism is *Staphylococcus aureus* and said nucleotide sequence is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

Claim 88 (canceled):

Claim 89 (previously presented): The method of Claim 12, wherein said sensitized cell is a Gram positive bacterium.

Claim 90 (previously presented): The method of Claim 89, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 91 (previously presented): The method of Claim 90, wherein said bacterium is *Staphylococcus aureus*.

Claim 92 (previously presented): The method of Claim 90, wherein said *Staphylococcus* species is coagulase negative.

Claim 93 (previously presented): The method of Claim 91, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 94 (previously presented): The method of Claim 12, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 95 (previously presented): The method of Claim 12, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 96 (previously presented): The method of Claim 12, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claims 97-99 (canceled):

Claim 100 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

- (a) providing a sublethal level of an antisense nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, wherein said antisense nucleic acid reduces the activity or amount of a gene product required for cellular proliferation, thereby producing a sensitized cell, provided that said sensitized cell is a prokaryotic organism;
- (b) contacting said sensitized cell with a compound; and
- (c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claim 101 (previously presented): The method of Claim 48, wherein said pathogenic microorganism is selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Listeria monocytogenes*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,

Staphylococcus epidermidis, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

Claim 102 (canceled):

Claim 103 (previously presented): The method of Claim 100, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enterococcus faecalis*.

Claim 104 (previously presented): The method of Claim 103, wherein said prokaryotic organism is *Staphylococcus aureus* and said antisense nucleic acid is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

Claim 105 (canceled).